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RAW SEQUENCE LISTING DATE: 10/04/2001 PATENT APPLICATION: US/09/885,478 TIME: 17:56:10

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\10042001\1885478.raw

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      3 <110> APPLICANT: SALON, JOHN A
             LAZ, THOMAS M
      5
             NAGORNY, RAISA
             WILSON, AMY E
      8 <120> TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR
(MCH1) AND
             USES THEREOF
    11 <130> FILE REFERENCE: 1795/57453-A-PCT-US
    13 <140> CURRENT APPLICATION NUMBER: 09/885,478
C--> 14 <141> CURRENT FILING DATE: 2001-09-24
    16 <150> PRIOR APPLICATION NUMBER: PCT/US99/31169
    17 <151> PRIOR FILING DATE: 1999-12-30
    19 <160> NUMBER OF SEQ ID NOS: 28
    21 <170> SOFTWARE: PatentIn version 3.1
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 1269
    25 <212> TYPE: DNA
    26 <213> ORGANISM: HOMO SAPIENS
    28 <400> SEOUENCE: 1
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    31 ggctgccagg ctacggagga agaccccctt cccgactgcg gggcttgcgc tccgggacaa
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    33 ggtggcaggc gctggaggct gccgcagcct gcgtgggtgg aggggagctc agctcggttg
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    35 tgggagcagg cgaccggcac tggctggatg gacctggaag cctcgctgct gcccactggt
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    37 cccaatgcca gcaacacctc tgatggcccc gataacctca cttcagcagg atcacctcct
                                                                             300
    39 cgcacgggga gcatctccta catcaacatc atcatgcctt cggtgttcgg caccatctgc
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    41 ctcctgggca tcatcgggaa ctccacggtc atcttcgcgg tcgtgaaqaa gtccaagctg
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    43 cactggtgca acaacgtccc cgacatette atcateaace teteggtagt agateteete
                                                                             480
    45 ttteteetgg geatgeeett eatgateeae eageteatgg geaatggggt gtggeaettt
                                                                             540
    47 ggggagacca tgtgcaccct catcacggcc atggatgcca atagtcagtt caccagcacc
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    49 tacatectga eegecatgge cattgacege tacetggeea etgtecacee catetettee
                                                                             660
    51 acgaagttcc ggaagccetc tgtggccacc ctggtgatct gcctcctgtg ggccctctcc
                                                                             720
    53 ttcatcagca tcacccctgt gtggctgtat gccagactca tccccttccc aggaggtgca
                                                                             780
    55 gtgggctgcg gcatacgcct gcccaaccca gacactgacc tctactggtt caccctgtac
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    57 cagtttttcc tggcctttgc cctqcctttt gtggtcatca caqccqcata cgtgaggatc
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    59 ctgcagcgca tgacgtcctc agtggccccc gcctcccagc gcagcatccg gctgcggaca
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    61 aagagggtga cccgcacagc catcgccatc tgtctggtct tctttgtgtg ctgggcaccc
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    63 tactatgtgc tacagetgac ecagttgtcc atcageegec egaceeteac etttgtctac
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    65 ttatacaatg cggccatcag cttgggctat gccaacagct gcctcaaccc ctttgtgtac
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    67 atcgtgctct gtgagacgtt ccgcaaacgc ttggtcctgt cggtgaagcc tgcagccag
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    69 gggcagette gegetgteag caaegeteag aeggetgaeg aggagaggae agaaagcaaa
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    76 <212> TYPE: PRT
    77 <213> ORGANISM: HOMO SAPIENS
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85 86	Gly	Gly	Gly	Ser 20	Gly	Cys	Gln	Ala	Thr 25	Glu	Glu	Asp	Pro	Leu 30	Pro	Asp
	Cys	Gly	Ala 35		Ala	Pro	Gly	Gln 40	Gly	Gly	Arg	Arg	Trp 45		Leu	Pro
93 94	Gln	Pro 50	Ala	Trp	Val	Glu	Gly 55	Ser	Ser	Ala	Arg	Leu 60	Trp	Glu	Gln	Ala
97 98		Gly	Thr	Gly	Trp	Met 70	Asp	Leu	Glu	Ala	Ser 75	Leu	Leu	Pro	Thr	Gly 80
101 102		Asn	Ala	Ser	Asn 85	Thr	Ser	Asp	Gly	Pro 90	Asp	Asn	Leu	Thr	Ser 95	Ala
105 106		Ser	Pro	Pro 100		Thr	Gly	Ser	: Ile 105		Tyr	Ile	Asr	Ile 110		Met
	Pro	Ser	Val	Phe		Thr	Ile	Cys 120	Leu		Gly	Ile	11e	Gly		Ser
113	Thr		Ile		Ala	Va1		Lys		ser	Lys		His		Суя	Asn
$\frac{114}{117}$		130 Val		Asp	Ile	Phe	135 Ile		. Asn	Leu	Ser	140 Val		Asp	Leu	Leu
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121 122	Phe	Leu	Leu	Gly	Met 165		Phe	Met	Ile	His 170		Leu	Met	Gly	Asn 175	Gly
125 126	Val	Trp	His	Phe 180		Glu	Thr	Met	Cys 185		Leu	Ile	Thr	Ala 190		Asp
129		Asn			Phe	Thr	Ser		Tyr		Leu	Thr		Met		Ile
130		7 ~~	195		31.	mh	1107	200		T1.	0		205		D1	3
134		210					215					220				Arg
	Lys 225		Ser	Val	Ala	Thr 230		Val	Ile	Cys	Leu 235		Trp	Ala	Leu	Ser 240
141 142	Phe	Ile	Ser	Ile	Thr 245	Pro	Val	Trp	Leu	Tyr 250		Arg	Leu	Ile	Pro 255	Phe
145 146	Pro	Gly	Gly	Ala 260	Val	G1y	Cys	Gly	11e 265	_	Leu	Pro	Asn	Pro 270	_	Thr
149	Asp	Leu		Trp	Phe	Thr	Leu		Gln		Phe	Leu		Phe		Leu
150	Dwo	Dho	275		T1.	m b so	<b>71</b>	280		17. 1	<b>3</b>	<b>T</b> 1.	285		3	34.4
154		290					295					300				Met
	Thr	Ser	Ser	Val	Ala	Pro 310	Ala	Ser	Gln	Arg	Ser 315	Ile	Arg	Leu	Arg	Thr 320
		Arg	Val	Thr	Arg		Ala	Ile	Ala	Ile		Leu	Val	Phe	Phe	
162					325					330	_				335	
165	Cys	Trp	Ala	Pro	Tyr	Tyr	Val	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser
166				340					345					350		
	Arg	Pro		Leu	Thr	Phe	Val		Leu	Tyr	Asn	Ala	Ala	Ile	Ser	Leu
170			355					360					365			
	Gly		Ala	Asn	Ser	Cys		Asn	Pro	Phe	Val		Ile	Va1	Leu	Cys
174		370			_	_	375		_	_		380				
		Thr	Phe	Arg	Lys		Leu	Val	Leu	Ser		Lys	Pro	Ala	Ala	
	385	Cl-	T 011	A 20.0	* 1 ~	390	C	7 ~ ~	7 1 <b>-</b>	C1-	395	31-	3	<b>a</b> 1	<b>03.</b>	400
тот	GTĀ	GTIJ	ьeu	Arg	ATG	٧d٢	ser	ASI	Ala	GTIJ	inr	ата	Asp	GIU	GTU	arg

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199 agggagtgtc tcctacatca acatcattat gccttccgtg tttggtacca tctgtctcct
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201 gggcatcgtg ggaaactcca cggtcatctt tgctgtggtg aagaagtcca agctacactg
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                                                                          300
203 gtgcagcaac gtccccgaca tcttcatcat caacctctct gtggtggatc tgctcttcct
205 gctgggcatg cctttcatga tccaccagct catggggaac ggcgtctggc actttgggga
                                                                          360
                                                                          420
207 aaccatgtgc accetcatca cagccatgga cgccaacagt cagttcacta gcacctacat
                                                                          480
209 cctgactgcc atgaccattg accgctactt ggccaccgtc caccccatct cctccaccaa
211 gttccggaag ccctccatgg ccaccctggt gatctgcctc ctgtgggcgc tctccttcat
                                                                          540
                                                                          600
213 cagtatcacc cctqtqtqqc tctacqccaq gctcattccc ttcccagggg gtgctgtggg
215 ctgtggcatc cgcctgccaa acccggacac tgacctctac tggttcactc tgtaccagtt
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217 tttcctggcc tttgcccttc cgtttgtggt cattaccgcc gcatacgtga aaatactaca
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221 gqtgacccgc acggccattg ccatctgtct ggtcttcttt gtgtgctggg caccctacta
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223 tgtgctqcag ctgacccagc tgtccatcag ccgcccgacc ctcacgtttg tctacttgta
225 caacgcggcc atcagcttgg gctatgctaa cagctgcctg aacccctttg tgtacatagt
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231 ctgacaattc cccagtcgcc tccaagtcag gccaccccat caaaccgtgg ggagagatac
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239 <211> LENGTH: 353
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                                    25
253 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
257 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
258
                            55
                                                 60
261 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
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                                             75
265 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
266
                                        90
269 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
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273 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
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277 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
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                        150
                                             155
285 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
                                         170
                    165
289 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
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                                     185
                180
293 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
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            195
297 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
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301 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
302 225
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305 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
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                                         250
309 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
                                     265
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313 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
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                                                     285
317 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
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321 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
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325 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
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340 <213> ORGANISM: ARTIFICIAL SEQUENCE
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352 <213> ORGANISM: ARTIFICIAL SEQUENCE
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355 <223> OTHER INFORMATION: PRIMER
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362 <211> LENGTH: 45
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364 <213> ORGANISM: ARTIFICIAL SEQUENCE 366 <220> FEATURE: 367 <223> OTHER INFORMATION: PROBE 369 <400> SEQUENCE: 7 370 ctcctgggca tgcccttcat gatccaccag ctcatgggca atggg 45 373 <210> SEQ ID NO: 8 374 <211> LENGTH: 25 375 <212> TYPE: DNA 376 <213> ORGANISM: ARTIFICIAL SEQUENCE 378 <220> FEATURE: 379 <223> OTHER INFORMATION: PRIMER 381 <400> SEQUENCE: 8 25 382 cttctaggcc tgtacggaag tgtta 385 <210> SEQ ID NO: 9 386 <211> LENGTH: 27 387 <212> TYPE: DNA 388 <213> ORGANISM: ARTIFICIAL SEQUENCE 390 <220> FEATURE: 391 <223> OTHER INFORMATION: PRIMER 393 <400> SEQUENCE: 9 394 gttgtggttt gtccaaactc atcaatg 27 397 <210> SEQ ID NO: 10 398 <211> LENGTH: 37 399 <212> TYPE: DNA 400 <213> ORGANISM: ARTIFICIAL SEQUENCE 402 <220> FEATURE: 403 <223> OTHER INFORMATION: PRIMER 405 <400> SEQUENCE: 10 406 cgcggatcca ttatgtctgc actccgaagg aaatttg 37 409 <210> SEQ ID NO: 11 410 <211> LENGTH: 38 411 <212> TYPE: DNA 412 <213> ORGANISM: ARTIFICIAL SEQUENCE 414 <220> FEATURE: 415 <223> OTHER INFORMATION: PRIMER 417 <400> SEQUENCE: 11 418 cgcgaattct tatgtgaagc gatcagagtt catttttc 38 421 <210> SEQ ID NO: 12 422 <211> LENGTH: 34 423 <212> TYPE: DNA 424 <213> ORGANISM: ARTIFICIAL SEQUENCE 426 <220> FEATURE: 427 <223> OTHER INFORMATION: PRIMER 429 <400> SEQUENCE: 12 34 430 gcgggatccg ctatggctgg tgattctagg aatg 433 <210> SEQ ID NO: 13 434 <211> LENGTH: 29 435 <212> TYPE: DNA 436 <213> ORGANISM: ARTIFICIAL SEQUENCE

VERIFICATION SUMMARY

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Output Set: N:\CRF3\10042001\1885478.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date